

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:08:26 ; Search time 82 Seconds  
(without alignments)  
892.033 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854  
Sequence: 1 MTSLSDTVEFTGTTSTYYDY.....LERTSVSPSTAPELSTVF 355

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1710	92.2	355	6	Q8WMR4
2	1709	92.2	355	6	Q8WMR5
3	1704	91.9	355	6	Q8BDS8
4	1376.5	74.2	358	6	Q8NOM0
5	1148	61.9	351	6	Q8MYU9
6	1128.5	60.9	355	6	Q8MYU8
7	1115.5	60.2	355	11	Q9JLY8
8	1115.5	60.2	355	11	Q9JLY9
9	958.5	51.7	383	12	Q89609
10	958	51.7	339	6	Q8TQU3
11	956	51.6	339	6	Q8TQU0
12	953.5	51.4	352	6	Q8YNC6
13	953.5	51.4	352	6	Q8YNC6
14	953	51.4	339	6	Q8YU48
15	952.5	51.4	352	6	Q8YU48
16	952	51.3	339	6	Q8YU48

17	952	51.3	339	6	Q8YU48	Q8YU48
18	947.5	51.1	352	6	Q8YU48	Q8YU48
19	947.5	51.1	352	6	Q8YU48	Q8YU48
20	947.5	51.1	352	6	Q8YU48	Q8YU48
21	947.5	51.1	352	6	Q8YU48	Q8YU48
22	946.5	51.1	352	6	Q8YU48	Q8YU48
23	945.5	51.0	352	6	Q8YU48	Q8YU48
24	944.5	50.9	352	6	Q8YU48	Q8YU48
25	944.5	50.9	352	6	Q8YU48	Q8YU48
26	944.5	50.9	352	6	Q8YU48	Q8YU48
27	943.5	50.9	352	6	Q8YU48	Q8YU48
28	943.5	50.9	352	6	Q8YU48	Q8YU48
29	942.5	50.8	352	6	Q8YU48	Q8YU48
30	942.5	50.8	352	6	Q8YU48	Q8YU48
31	942.5	50.8	352	6	Q8YU48	Q8YU48
32	941.5	50.8	352	6	Q8YU48	Q8YU48
33	941.5	50.8	352	6	Q8YU48	Q8YU48
34	941.5	50.8	352	6	Q8YU48	Q8YU48
35	941.5	50.8	352	6	Q8YU48	Q8YU48
36	940.5	50.7	352	6	Q8YU48	Q8YU48
37	940.5	50.7	352	6	Q8YU48	Q8YU48
38	940.5	50.7	352	6	Q8YU48	Q8YU48
39	940.5	50.7	352	6	Q8YU48	Q8YU48
40	939.5	50.7	352	6	Q8YU48	Q8YU48
41	939.5	50.7	352	6	Q8YU48	Q8YU48
42	939.5	50.7	352	6	Q8YU48	Q8YU48
43	939.5	50.7	352	6	Q8YU48	Q8YU48
44	938.5	50.6	352	6	Q8YU48	Q8YU48
45	938.5	50.6	352	6	Q8YU48	Q8YU48

#### ALIGNMENTS

##### RESULT 1

Q8WMR4 PRELIMINARY; PRT; 355 AA.  
ID Q8WMR4;  
AC Q8WMR4;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DR 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Chemokine receptor 3.  
GN CCR3.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Iino T., Chu D., Sugimoto H., Kannan Y., Matanabe A., Liu N.,  
RA Bacon K.B.;  
RT "Cloning and characterization of cynomolgus monkey CCR3.";  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AY065647; AL55443.1;  
DR InterPro: IPR000276; GPCR\_Rhodopsin.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsin.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; UNKNOWN\_1.  
DR PROSITE: PS0262; G-PROTEIN\_RECEP\_FL\_2; 1.  
KW Receptor.  
SQ SEQUENCE 355 AA; 40793 MW; F3228C6835A1A830 CRC64;

Query Match 92.2% Score 1710; DB 6; Length 355;  
Best local similarity 91.8%; Pred. No. 7.8e-143;  
Matches 326; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTSLSDTVEFTGTTSTYYDYGLCEKADTRALMQFPPPLSLVFTVGLGNVVMILI 60  
DB 1 MTSLSDTVEFTGTTSTYYDYGLCEKADTRALMQFPPPLSLVFTVGLGNVVMILI 60  
QY 61 KYRRLRTMTNTYLLNLALISDLFLVLTLPFWIHYRGHNVGRCMKLLISFTTGIXSE 120  
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Db 61 KYRRLRMNTNYLLMLAISDLLEFTLPFWIHVVERRMVSHGCKVLSGTYHTGLYSE 120
Qy 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Db 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Qy 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Db 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Qy 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Db 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Qy 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355
Db 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355

RESULT 2
Q9BWR5 PRELIMINARY: PRT: 355 AA.
ID 08WNR5;
AC 08WNR5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DR 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chemokine receptor 3.
OS CCR3.
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Iino T., Chu D., Sugimoto H., Kannan Y., Watanabe A., Liu N.,
RA Bacon K.B.;
RT "Cloning and characterization of cynomolgus monkey CCR3.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY065646; AAL5442.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA: 40779 MW: 328BDE21D032201 CRC64;

Query Match 92.2%; Score 1709; DB 6; Length 355;
Best Local Similarity 91.5%; Pred. No. 9.6e-143;
Matches 325; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTSIDVTEGTSTYDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMVMI 60
Db 1 MTSIDVTEGTSTYDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMVMI 60
Qy 61 KYRRLRMNTNYLLMLAISDLLEFTLPFWIHVVERRMVSHGCKVLSGTYHTGLYSE 120
Db 61 KYRRLRMNTNYLLMLAISDLLEFTLPFWIHVVERRMVSHGCKVLSGTYHTGLYSE 120
Qy 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Db 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Qy 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Db 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Qy 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Db 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Qy 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355
Db 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355

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Db 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355
Qy 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355

RESULT 3
Q9BDS8 PRELIMINARY: PRT: 355 AA.
ID 09BDS8;
AC 09BDS8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DR 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Chemokine receptor CCR3.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21134756; PubMed-11242524;
RA Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and str133;
RT potential coreceptors for HIV type 1, HIV type 2, and SIV.";
RL AIDS Res. Hum. Retroviruses 17:371-375(2001).
DR EMBL; AF291668; AAK25739.1;
DR HSPR; P02699; 1F88.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA: 40914 MW: 287865A177D261CE CRC64;

Query Match 91.9%; Score 1704; DB 6; Length 355;
Best Local Similarity 91.8%; Pred. No. 2.6e-142;
Matches 326; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MTSIDVTEGTSTYDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMVMI 60
Db 1 MTSIDVTEGTSTYDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMVMI 60
Qy 61 KYRRLRMNTNYLLMLAISDLLEFTLPFWIHVVERRMVSHGCKVLSGTYHTGLYSE 120
Db 61 KYRRLRMNTNYLLMLAISDLLEFTLPFWIHVVERRMVSHGCKVLSGTYHTGLYSE 120
Qy 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Db 121 IFFIILLTIDRLAIVAHVAFALRARTVTEGVTISVTWGLAVLAALPERIFETEELPEE 180
Qy 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Db 181 TLCSALYEDPDYVYSRHHFTLMTIFCLVPLPLVNAICTGTIKTLRCPSSKKKKAIRL 240
Qy 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Db 241 IFVIAVFEFTWTPYNAVALISYSQSLFNCDCSKSHLDVMTVEVIAVSHCCMNPVI 300
Qy 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355
Db 301 YAFVGERFRKYLRFHFRHMLHGLGRYIPFLPSEKLERISSVSPSTAPELSTIVF 355

RESULT 4
Q9NOMO PRELIMINARY: PRT: 358 AA.
ID 09NOMO;
AC 09NOMO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DR 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CCR3 receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wolfe G.C., Mudgett J.S.;  
 RT "Cloning and characterization of the sheep CCR3 receptor."  
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF266468; AAF71786.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPS.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 358 AA; 40985 MW; 2B54F9128590181E CRC64;  
 Query Match 74.28; Score 1376.5; DB 6; Length 358;  
 Best Local Similarity 73.38; Pred. No. 2e-113;  
 Matches 263; Conservative 41; Mismatches 50; Indels 5; Gaps 2;  
 QY 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFPPPLYSVFTVGLGNVNVV 56  
 DB 1 MANSVQIEITVEAGTTPYDYGALPCEKSNKELAAQFLPLSLVFMIGLGNVNVV 60  
 QY 57 MILIKRRLIMNTIYLNLAIISDLFLVLPFWIHVGHNNVFGHCKLLSGFYHTG 116  
 DB 61 VILTKKRLIMNTIYLNLAIISDLFLVLPFWIHVGHNNVFGHCKLLSGFYHTG 120  
 QY 117 LYSIEPFIILTDRIYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 176  
 DB 121 LYSIEPFIILTDRIYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 180  
 QY 177 LFEETLCSALYPEDTVYSNRHFTLRMTIFCLVPLLVMAICYTGIIKTLRCPSKRYK 236  
 DB 181 EAGLTICSPLYPENNVAMKQFALRNNIIGLALPLLVMAVCYSGIITKTLRCPSKRYK 240  
 QY 237 AILILFVMAVFETFPYVAVALLISYOSILFGNDCERKHLDVNLVTEVLAHSCKM 296  
 DB 241 AILILFVMAVFETFPYVAVALLISYOSILFGNDCERKHLDVNLVTEVLAHSCKM 299  
 QY 297 NPVIYAVGGRFRKYLHFFRHLLMLHGRYIPFLPSEKLEERTSVSPSTAEPESLIVE 355  
 DB 300 NPVIYAVGGRFRKYLHFFRHLLMLHGRYIPFLPSEKLEERTSVSPSTAEPESLIVE 358  
 RESULT 5  
 Q9MYJ9 PRELIMINARY; PRT; 351 AA.  
 ID Q9MYJ9  
 AC Q9MYJ9  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Chemokine receptor.  
 GN CCR1  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20153429; PubMed-10686294;  
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,  
 RA Ghanam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,  
 RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;  
 RT "Species selectivity of a small molecule antagonist for the CCR1  
 chemokine receptor."  
 RL Eur. J. Pharmacol. 389:41-49(2000).  
 DR EMBL: AF127527; AAF36452.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPS.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;

DR PROSITE: PS50262; G\_PROTEIN\_RECPR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;  
 Query Match 61.98; Score 1148; DB 6; Length 351;  
 Best Local Similarity 62.18; Pred. No. 2.7e-93;  
 Matches 221; Conservative 54; Mismatches 75; Indels 6; Gaps 3;  
 QY 1 MTSLSLDTVEFETGTSYDDVGLCEKADTRALMAQFPPPLYSVFTVGLGNVNVV 59  
 DB 1 MTSATTTDDTTEYEDTTPCQKVAVARAFAGQGLPLPLSLVFTVGLGNVNVV 59  
 QY 60 IKTRRLIMNTIYLNLAIISDLFLVLPFWIHVGHNNVFGHCKLLSGFYHTG 119  
 DB 60 MKYKRLIMNTIYLNLAIISDLFLVLPFWIHVGHNNVFGHCKLLSGFYHTG 119  
 QY 120 EIFEPIILTDRIYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 179  
 DB 120 EVFPIILTDRIYLAIVHAFALRAFTVGVTSIYTWGLAVLAALPEFETEE 179  
 QY 180 ETLCALYPEDTVYSNRHFTLRMTIFCLVPLLVMAICYTGIIKTLRCPSKRYK 239  
 DB 180 HYSCLHFPHESLRQWFOFALKNLNIGLVPLLVMAVCYSGIITKTLRCPSKRYK 239  
 QY 240 LIFVMAVFETFPYVAVALLISYOSILFGNDCERKHLDVNLVTEVLAHSCKM 299  
 DB 240 LIFVMAVFETFPYVAVALLISYOSILFGNDCERKHLDVNLVTEVLAHSCKM 299  
 QY 300 IYAVGGRFRKYLHFFRHLLMLHGRYIPFLPSEKLEERTSVSPSTAEPESLIVE 355  
 DB 300 IYAVGGRFRKYLHFFRHLLMLHGRYIPFLPSEKLEERTSVSPSTAEPESLIVE 351  
 RESULT 6  
 Q9MYJ8 PRELIMINARY; PRT; 355 AA.  
 ID Q9MYJ8  
 AC Q9MYJ8  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Chemokine receptor.  
 GN CCR1  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
 OX NCBI\_TaxID=9483;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20153429; PubMed-10686294;  
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,  
 RA Ghanam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,  
 RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;  
 RT "Species selectivity of a small molecule antagonist for the CCR1  
 chemokine receptor."  
 RL Eur. J. Pharmacol. 389:41-49(2000).  
 DR EMBL: AF127528; AAF36453.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPS.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPR\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPR\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;  
 Query Match 60.98; Score 1128.5; DB 6; Length 355;  
 Best Local Similarity 60.68; Pred. No. 1.4e-91;  
 Matches 215; Conservative 56; Mismatches 77; Indels 7; Gaps 1;  
 QY 8 VEPGTSYDDV-----GLCEKADTRALMAQFPPPLYSVFTVGLGNVNVV 60  
 DB 1 MTSATTTDDTTEYEDTTPCQKVAVARAFAGQGLPLPLSLVFTVGLGNVNVV 60  
 QY 61 KYRRLIMNTIYLNLAIISDLFLVLPFWIHVGHNNVFGHCKLLSGFYHTG 120

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DB 61 QYKRLAKNTSTYLLMLAISDLLEFTLPWISYQKTDWVGNACKVLSGYTYGLISE 120
QY 121 IFFIILLTIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYEETELREE 180
DB 121 IFFIILLTIDRYLAIVHAFALRARTVFGVITSIIIMWLATIASLPGLYFAKQWEITH 180
QY 181 TLCSALYEDPDYYSNRHHTLMFTFCVLVPLLVNAICYTGIIKLLRCPSSKKYKAIRL 240
DB 181 RTCSLHPHESKOEKRLQALKNLGLVLPPLVAVICYTGIIKLLRPNKSKKAVL 240
QY 241 IFVIAVFEIEMTPYNAVALISYSOSILEGNDCEKSHLDVLMVTEVAYSHCCMNPYI 300
DB 241 IFVIMIIFFELMTYFNLTLLISVDFLETTYCEBGRQDLAIQVTEMAIYTHCCVNPYI 300
QY 301 YAFVGERFRKYLHFFHRLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSVF 355
DB 301 YAFVGERFRKRLQFHRRAVAVLWKMLPFLSVDBLERASSVSPSTGEHVSAGF 355

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## RESULT 7

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Q9JLY8 PRELIMINARY; PRT; 355 AA.
AC Q9JLY8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Macrophage inflammatory protein-1 alpha receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD;
RC MEDLINE=20555330; PubMed=11091494;
RA Waller A., Nayee P., Czaplowski L.G.;
RT Identification and characterization of a rat macrophage inflammatory
RT protein-1 alpha receptor.
RL J. Hematother. Stem Cell Res. 9:703-710(2000).
DR EMBL; AF119381; AAF34340.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA; 40838 MW; 2FEB8661D1E6075 CRC64;

```

Query Match 60.2%; Score 1115.5; DB 11; Length 355;  
 Best Local Similarity 58.6%; Pred. No. 2e-90; Indels 1; Gaps 1;  
 Matches 202; Conservative 66; Mismatches 76;

```

QY 9 ETEFGTSTYD-DVGLLCEKADTRALMAQVPPVLSYFVGLGNVVMILIKYRLRI 67
DB 8 EYPTTETXDYDSDPPCQKTAVRAGAGLPLPSYFVLIQVGNLIVLVMQHRRLQS 67
QY 68 MTNITLNLAIISDLLEFTLPWIMHYVGNHNVFGHGMCKLSGYHTGLYSEIIFI 127
DB 68 MTSITLFLNLAASDLVLEFTLPWIMDYKLDNMVFGDAMCKLSGFTYGLYSEIIFI 127
QY 128 TIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYEETELFEETLSALY 187
DB 128 TIDRYLAIVHAFALRARTVFGVITSIIIMWLATIASLPALCFKAEWFEHHCSPHF 187
QY 188 PEDVYSNRHHTLMFTFCVLVPLLVNAICYTGIIKLLRCPSSKKYKAIRLIVYAV 247
DB 188 PDESILTKWRKQALKNLNLGLILPLVMICYAGIIRILRPNKSKKAAVALIRLAIITL 247
QY 248 FFIFETPYNVALISYSOSILEGNDCEKSHLDVLMVTEVAYSHCCMNPYIYAVGER 307
DB 248 FFLMTPYNLVYVSAFQDVLETTNOCESKQDLAIQVTEVAYTHCCVNPITYVVGSR 307

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QY 308 FRKYLRHRLMLHGRYIPFLPSEKLERTSSVSPSTAEPLS 352
DB 308 FRKYLRQLEFRHVAIPLAKMLPFSVDLERTSSVSPSTGEHLS 352

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## RESULT 8

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Q91VP9 PRELIMINARY; PRT; 355 AA.
AC Q91VP9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chemokine (C-C) receptor 1.
GN CMKRL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011092; AAH11092.1; -.
DR MGD; MGI:104618; Cmkbr1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 355 AA; 40894 MW; 41B0D566A56BC4F7 CRC64;

```

Query Match 60.2%; Score 1115.5; DB 11; Length 355;  
 Best Local Similarity 58.7%; Pred. No. 2e-90;  
 Matches 206; Conservative 62; Mismatches 82; Indels 1; Gaps 1;

```

QY 6 DVEIFGTSTYD-DVGLLCEKADTRALMAQVPPVLSYFVGLGNVVMILIKYRR 64
DB 5 DTEAVPTTETXDYDSDPPCQKTAVRAGAGLPLPSYFVLIQVGNLIVLVMQHRRL 64
QY 65 IRTNITLNLAIISDLLEFTLPWIMHYVGNHNVFGHGMCKLSGYHTGLYSEIIFI 124
DB 65 IQSMSTYFLNLAASDLVLEFTLPWIMDYKLDNMVFGDAMCKLSGFTYGLYSEIIFI 124
QY 125 ILLTIDRYLAIVHAFALRARTVFGVITSIVTWGLAVLAALPEFIYEETELFEETLS 184
DB 125 ILLTIDRYLAIVHAFALRARTVFGVITSIIIMWLATIASLPALCFKAEWFEHHCSPHF 184
QY 185 ALYEDPDYYSNRHHTLMFTFCVLVPLLVNAICYTGIIKLLRCPSSKKYKAIRLIVY 244
DB 185 PHFPYKSLKQWRKQALKNLNLGLILPLVMICYAGIIRILRPNKSKKAAVALIRLAI 244
QY 245 MAVFIFETPYNVALISYSOSILEGNDCEKSHLDVLMVTEVAYSHCCMNPYIYAV 304
DB 245 TLLFPLMTPYNLVYVSAFQDVLETTNOCESKQDLAIQVTEVAYTHCCVNPITYV 304
QY 305 GERFRKYLHFFHRLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSVF 355
DB 305 GERFRKYLHFFHRLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSVF 355

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## RESULT 9

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Q89609 PRELIMINARY; PRT; 383 AA.
AC Q89609;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE G protein-coupled receptor.
OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=82831;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95302501; PubMed-77832207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2."
RL J. Mol. Biol. 249:520-528(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Telford E.A.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20824; AAC13866.1; -
DR EMBL: U20824; AAC13788.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PS50262; G_PROTEIN_RECIP_FL_2; 1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
SQ SEQUENCE 383 AA; 43667 MW; 0C65C53EAF539F72 CRC64;

Query Match 51.7%; Score 958.5; DB 12; Length 383;
Best Local Similarity 50.8%; Pred. No. 1.5e-76;
Matches 183; Conservative 63; Mismatches 87; Indels 29; Gaps 3;

QY 2 TTSIDVETFGTTS-----YDDV-----GLCEKADTRALM 33
DB 12 TSSLATMTNTPISLTSVTTTASVPTNSSDDYDDDDVDYVESAPCYKSDTRRLA 71
QY 34 AQVPPYLSLVETVGLGNVVMILIKYRLRIMNIIYLNLAISDLLEFVLPFWIHY 93
DB 72 AOVVPAIYLLVLEFGLGNLIVIVIRYMKIKMLNMLNLNLAISDLLEFVLPFWIHY 131
QY 94 V-RGNMNVFGHCKILSGFYHGTGSEIFPIILLTDRIYAIYHAPALBARVTVGVI 152
DB 132 IGMHTDFTFGISLCKLRGVCYMSLYSOVFCILLTVDRILAVYAVATLFRVTVGIV 191
QY 153 TSVITGIAVLAALPEEFYETELFEETLCSALYPERVYSNRHFTLRMTICLVPL 212
DB 192 TCVCWTWLAGLSLPEFFGHODNGRQCDPRYPKSTWWRRAHAKYIMLSLILPL 251
QY 213 LVNAICTGTGIIKTLKCPSSKKRYKARILFIYMAVFIETWPNVAILSSYOSILFGND 272
DB 252 LIMAVCYVILIRLLRRSPKKRYKARILFIYMAVFEWPPYVILLSTFHTLMIQ 311
QY 273 CERSKHLDVNLVTEVAIYSHCCNRPYIYAVGGRFRKYLHFRHRLHMLGRIYPLP 332
DB 312 CASSNIDMALILRTYVATHCCINPIYIAVGVGKFRHLHFHTYVAILCRYIPLS 371
QY 333 SE 334
DB 372 GD 373

RESULT 10
Q9TQ03 PRELIMINARY; PRT; 339 AA.
AC Q9TQ03;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kulkarni C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -

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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
RW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38712 MW; 8A2DD074093A56AE CRC64;

Query Match 51.7%; Score 958; DB 6; Length 339;
Best Local Similarity 55.8%; Pred. No. 1.5e-76;
Matches 188; Conservative 55; Mismatches 88; Indels 6; Gaps 5;

QY 17 YD-DVGLT--CEKADTRALMAQVPPYLSLVETVGLGNVVMILIKYRLRIMNTNYL 73
DB 3 YDIDYGLSEPOKIDIVKRIANQPLPLSLVIFIGLVGNMLVLLINCKIKLSKSTDIYL 62
QY 74 LNLAISDLLEFVLPFWIHYVGRHNVFGHCKILSGFYHGTGSEIFPIILLTDRIYL 133
DB 63 LNLAISDLLEFVLPFWIHYVGRHNVFGHCKILSGFYHGTGSEIFPIILLTDRIYL 121
QY 134 AIVHAFALRARTVFGYITSLVITGLVLAALPEEFYETELFEETLCSALYPERVY 193
DB 122 AIVHAFALRARTVFGYITSLVITGLVLAALPEEFYETELFEETLCSALYPERVY 181
QY 194 SWRHEHTLRMTICLVPLVLAICVYTIKTLKCPSSKKRYKARILFIYMAVFIETW 252
DB 182 FKNRQGLKMLVGLVLEPLLVINVCYSGILTKTLKCRERKRRKRAVRLIFIMYVFLW 241
QY 253 TPYVNAIILSSYOSILFENDCERSKHLDVNLVTEVAIYSHCCNRPYIYAVGGRFRKYL 312
DB 242 APYVNVLLNTPPEFFGLNDSSNGLDQAQVETLGMTCCINPIYVAVGVGKFRYI 301
QY 313 RHFHRLHMLGRIYPLPSEKLERTSSV-SPSTAE 348
DB 302 LDFRKHIAKFPCKCQPFQREVPGRGSSVYTRISGE 338

RESULT 11
Q9TQ03 PRELIMINARY; PRT; 339 AA.
AC Q9TQ03;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kulkarni C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162014; AAD47769.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
RW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 51.6%; Score 956; DB 6; Length 339;
Best Local Similarity 55.8%; Pred. No. 2.2e-76;
Matches 188; Conservative 54; Mismatches 89; Indels 6; Gaps 5;

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```

OY 17 YD-DVGLL--CEKADTRALMAQFPPPLYSLVFTVGLGNVVVMIILIKYRRLIMNTIYL 73
DB 3 YDIDYGLSEPOCKIDVKRIIAOQLPPLYSLVFTVGLGNVMIIVLILNCKRKLSMTDITL 62
OY 74 LNLAIISDLLEFVTLPEFMIHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRL 133
DB 63 LNLAIISDLLEFVTLPEFMIHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRL 121
OY 134 AIVHAVPALRATVTEFVGLVAVLALPEFIEFEELFEETLCSALYEDPVY 193
DB 122 AIVHAVPALRATVTEFVGLVAVLALPEFIEFEELFEETLCSALYEDPVY 181
OY 194 SWRHHTLRATIFECVLEPLVMAIYTGIIITLLRC-PSKKYKARILFIYMAVFFIEM 252
DB 182 FWNKQTLKMLVGLVPLVAVICYSGLIKTLRCREKRRKRAVRLIFALIMYFLFM 241
OY 253 TPYNAVAILSSYOSTILFGNDCRSKHLDMVLTVEVIYASHCCMPVIAFGEFRKYL 312
DB 242 APYNAVAILNTPEFPGINDCSSNGLDQAMQVTLTGKHCINPVYAFGEFRKYL 301
OY 313 RHFFRHLMHLAGRYIPLPSEKLEKRTSSV-SPSTAE 348
DB 302 LDFPHKILAKPCKCCPVQREVPERGSSVYTRSTGE 338

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## RESULT 12

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O95NC6 PRELIMINARY; PRT; 352 AA.
AC 095NC6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Trechypithecus Johnii (hooded leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=66063;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF171883; AAK43366.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40462 MW; 52824E0322559F7F CRC64;

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Query Match 51.4%; Score 953.5; DB 6; Length 352;
Best Local Similarity 54.5%; Pred. No. 3.8e-76;
Matches 181; Conservative 58; Mismatches 90; Indels 3; Gaps 3;

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OY 24 CEKADTRALMAQFPPPLYSLVFTVGLGNVVVMIILIKYRRLIMNTIYLNLAIISDLF 83
DB 20 CQKINVKQIAARLPLPLYSLVFTVGLGNVMIIVLILNCKRKLSMTDITLNLAIISDLF 79
OY 84 LVTLPFWLHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRLAIVHAVPALR 143
DB 80 LVTLPFWLHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRLAIVHAVPALR 138
OY 144 ARTVFGVTSIVTWGLAVLALPEFIEFEELFEETLCSALYEDPVYSWRHHTLRM 203
DB 139 ARTVFGVTSIVTWGLAVLALPEFIEFEELFEETLCSALYEDPVYSWRHHTLRM 198
OY 204 TIFCVLPLVMAIYTGIIITLLRCPS-KKKYKARILFIYMAVFFIEMPYNAAILLS 262
DB 199 VILGIVLPLVAVICYSGLIKTLRCREKRRKRAVRLIFITIMYFLFMAYINIVLLIN 258

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OY 263 SYOSTILFGNDCRSKHLDMVLTVEVIYASHCCMPVIAFGEFRKYL RHFFRHLM 322
DB 259 TQGEFGLNCCSSNRLDQAMQVTLTGKHCINPVYAFGEFRKYL RHFFRHLM 318
OY 323 HLGRIYPLPSEKLEKRTSSV-SPSTAEPLST 353
DB 319 HFCKCSTIQDAPERASSVYTRSTGEDEISV 350

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## RESULT 13

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O97975 PRELIMINARY; PRT; 352 AA.
AC 097975:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor type 5.
GN CCR5.
OS Macaca arctoides (Stump-tailed macaque), and
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9540, 9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates."
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF075450; AAD19862.1; -.
DR EMBL; AF075449; AAD19861.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40521 MW; 5F276C85909FACB2 CRC64;

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Query Match 51.4%; Score 953.5; DB 6; Length 352;
Best Local Similarity 54.8%; Pred. No. 3.8e-76;
Matches 182; Conservative 58; Mismatches 89; Indels 3; Gaps 3;

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```

OY 24 CEKADTRALMAQFPPPLYSLVFTVGLGNVVVMIILIKYRRLIMNTIYLNLAIISDLF 83
DB 20 CQKINVKQIAARLPLPLYSLVFTVGLGNVMIIVLILNCKRKLSMTDITLNLAIISDLF 79
OY 84 LVTLPFWLHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRLAIVHAVPALR 143
DB 80 LVTLPFWLHYVGRHNVGHCCKILSGFYHTGLXSEIFITLLIDRLAIVHAVPALR 138
OY 144 ARTVFGVTSIVTWGLAVLALPEFIEFEELFEETLCSALYEDPVYSWRHHTLRM 203
DB 139 ARTVFGVTSIVTWGLAVLALPEFIEFEELFEETLCSALYEDPVYSWRHHTLRM 198
OY 204 TIFCVLPLVMAIYTGIIITLLRCPS-KKKYKARILFIYMAVFFIEMPYNAAILLS 262
DB 199 VILGIVLPLVAVICYSGLIKTLRCREKRRKRAVRLIFITIMYFLFMAYINIVLLIN 258
OY 263 SYOSTILFGNDCRSKHLDMVLTVEVIYASHCCMPVIAFGEFRKYL RHFFRHLM 322
DB 259 TQGEFGLNCCSSNRLDQAMQVTLTGKHCINPVYAFGEFRKYL RHFFRHLM 318
OY 323 HLGRIYPLPSEKLEKRTSSV-SPSTAEPLST 353
DB 319 HFCKCSTIQDAPERASSVYTRSTGEDEISV 350

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## RESULT 14

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O9TUS4 PRELIMINARY; PRT; 339 AA.
ID 09TUS4:
AC 09TUS4:

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01-MAY-2000 (Tremblrel.13, Created)  
01-MAY-2000 (Tremblrel.13, Last sequence update)  
01-JUN-2001 (Tremblrel.17, Last annotation update)  
C-C chemokine receptor 5 (Fragment).  
CCR5.  
Lemur variegatus (Ruffed lemur) (Varecia variegata).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Varecia.  
NCBI\_TaxID=9455;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
RA Shihata R., Yoder A., Pillai S., Kuiken C., Marx P., Molinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
species."  
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF162009; AAD47764.1; -  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm.1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G\_PROTEIN\_RECIP\_FL\_1; UNKNOWN\_1.  
DR RECEPTOR.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 339 AA; 38664 MW; B53CFE4E6B09E1A CRC64;  
Query Match 51.4%; Score 953; DB 6; Length 339;  
Best Local Similarity 55.8%; Pred. No. 4.1e-76;  
Matches 188; Conservative 54; Mismatches 89; Indels 6; Gaps 5;  
QY 17 YD-DVGL--CEKADTRALMAQFVPLYSLVFTVGLGNVVMILIKYRLRMTNTIYL 73  
DB 3 YDIDIGSEPCQCKIDVKRIAQQLPLYSIVFIFGLVGNMVLTLINCKRLKSMTDIYL 62  
QY 74 LNLASDLFLVLPFEMVHYRGHNVYFGHGMCKLSGFYHTGLYSEFFIILLIDRYL 133  
DB 63 LNLASDLFLVLPFEMVHYRGHNVYFGHGMCKLSGFYHTGLYSEFFIILLIDRYL 121  
QY 134 AIVAVPALRAVTFVGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDIVY 193  
DB 122 AIVAVPALRAVTFVGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDIVY 181  
QY 194 SMRFHRLKMTIFCLVPLVMAICYGIITLLRCS-KKRYAIRLIFYIMAVFLEW 252  
DB 182 FKKFQPLKMLVGLVPLVMAICYGIITLLRCS-KKRYAIRLIFYIMAVFLEW 241  
QY 253 TPYVAILLSYOSILRGNDERSKHLVMTLVETVIAVSHCCNPPYVAVGGERKYL 312  
DB 242 APYIVILLNTFPFEGFGLNDCSSNGLDQAMQVETETGMCINPVYAVGGERKYL 301  
QY 313 RHFFHRLMLHGLRYIPLPESEKLETTSSV-SPSTAE 348  
DB 302 LDFPHKHAIRPFCCKCPVFGREYVERGSSVYTRSTGE 338  
RESULT 15  
Q9TV48 PRELIMINARY; PRT; 352 AA.  
AC Q9TV48;  
DT 01-MAY-2000 (Tremblrel.13, Created)  
DT 01-MAY-2000 (Tremblrel.13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel.17, Last annotation update)  
DE CC chemokine receptor type 5.  
GN CCR5.  
OS Cercopithecus aesculans (black-cheeked white-nosed monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=36223;  
ON [1]  
RN RP SEQUENCE FROM N.A.  
RC STRAIN-52;

MEDLINE-99335215; PubMed-10408730;  
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,  
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;  
RT "Mutations in CCR5-coding sequences are not associated with HIV  
carrier status in African nonhuman primates."  
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-52;  
RA Muller-Trutwin M.C., Corbet S., Hansen J., Diop O.,  
RA Georges-Courbot M.C., Barre-Sinoussi F., Fomsgaard A.;  
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF035216; AAD44009.1; -  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm.1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G\_PROTEIN\_RECIP\_FL\_1; UNKNOWN\_1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECIP\_FL\_2; 1.  
KW RECEPTOR.  
SQ SEQUENCE 352 AA; 40650 MW; 7906236AA3945266 CRC64;  
Query Match 51.4%; Score 952.5; DB 6; Length 352;  
Best Local Similarity 54.5%; Pred. No. 4.7e-76;  
Matches 181; Conservative 58; Mismatches 90; Indels 3; Gaps 3;  
QY 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMILIKYRLRMTNTIYLNLASDLLE 83  
DB 20 COKINVKQIAARLLPLYSIVFIFGVGNILVLLINCKRLKSMTDIYLLNLASDLLE 79  
QY 84 LVTLPFVHYRGHNVYFGHGMCKLSGFYHTGLYSEFFIILLIDRYLAIVAVPALR 143  
DB 80 LVTLPFVHYRGHNVYFGHGMCKLSGFYHTGLYSEFFIILLIDRYLAIVAVPALR 138  
QY 144 ARTVFGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDIVYSMRPHRLM 203  
DB 139 ARTVFGVITSIYVGLAVLAALPEFIEETEELFEETLCSALYPEDIVYSMRPHRLM 198  
QY 204 TIFCLVPLVMAICYGIITLLRCS-KKRYAIRLIFYIMAVFLEWTPYVAILLS 262  
DB 199 TIFCLVPLVMAICYGIITLLRCS-KKRYAIRLIFYIMAVFLEWTPYVAILLS 258  
QY 263 SYOSILRGNDERSKHLVMTLVETVIAVSHCCNPPYVAVGGERKYLHFRHRLM 322  
DB 259 TFEFFGLNDCSSNRDLQAMQVETETGMCINPVYAVGGERKYLHFRHRLM 318  
QY 323 HLGRYIPLPESEKLETTSSV-SPSTAEDELSI 353  
DB 319 RFCKCSIFQGEAPERASSVYTRSTGEDEISV 350

Search completed: June 27, 2003, 18:14:28  
Job time : 84 secs

